

RA TUSHINSKI R.J., MOCHIZUKI D.Y., LARSEN A., GRABSTEIN K., COSMAN D.;
 RL PROC. NATL. ACAD. SCI. U.S.A. 82:6250-6254 (1985).
 RN [4]

RP SEQUENCE FROM N.A.

RM 85218749
 RA WONG G.G., WITEK J.S., TEMPLE P.A., WILKENS K.M., LEARY A.C.,
 RA LUXENBERG D.P., JONES S.S., BROWN E.L., KAY R.M., ORR E.C.,
 RA SHOMAKER C., GOLDE D.W., KAUFMAN R.J., HEWICK R.M., WANG E.A.,
 RA CLARK S.C.;
 RL SCIENCE 228:810-815 (1985).
 RN [5]

RP SEQUENCE FROM N.A.

RM 86030234
 RA MIYATAKE S., OTSUKA T., YOKOTA T., LEE F., ARAI K.-I.;
 RL EMBO J. 4:2561-2568 (1985).
 RN [6]

RP X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS).
 RM 97108420

RA DIENERICH K., BOONE T., KARPLUS P.A.;
 RL SCIENCE 254:1779-1782 (1991).
 RN [7]

RP X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS).
 RM 92235844

RA WALTER M.R., COOK W.J., EALICK S.E., NAGABHUSHAN T.L., TROTTER P.P.,
 RA BUGG C.E.;
 RL J. MOL. BIOL. 224:1075-1085 (1992).
 CC -!- FUNCTION: GRANULOCYTE/MACROPHAGE COLONY-STIMULATING FACTORS ARE

CC CYTOKINES THAT ACT IN HEMATOPOIESIS BY CONTROLLING THE PRODUCTION,
 CC DIFFERENTIATION, AND FUNCTION OF 2 RELATED WHITE CELL POPULATIONS
 CC OF THE BLOOD, THE GRANULOCYTES AND THE MONOCYTES-MACROPHAGES.
 CC -!- FUNCTION: STIMULATES THE GROWTH AND DIFFERENTIATION OF

CC HEMATOPOIETIC PRECURSOR CELLS FROM VARIOUS LINEAGES, INCLUDING
 CC GRANULOCYTES, MACROPHAGES, EOSINOPHILS AND ERYTHROCYTES.
 CC -!- SUBUNIT: MONOMER.

DR EMBL; M13207; HSCSFGMA.
 DR EMBL; M11734; HSCSFGMB.

DR EMBL; M11220; HSCMGSPA.

DR EMBL; X03021; HSCMGSEF.

DR EMBL; M10663; HSCSFGM.

DR PIR; A01853; FQHUGM.

DR PIR; C24636; C24636.

DR PIR; A25169; A25169.

DR PDB; 1CSG; 31-JAN-94.

DR PDB; 1GWF; 31-OCT-93.

DR MIM; 138960; 11TH EDITION.

DR PROSITE; PS00702; GM CSF.

KW CYTOKINE; GROWTH FACTOR; GLYCOPROTEIN; SIGNAL; 3D-STRUCTURE;
 KW POLYMORPHISM.

FT SIGNAL 1 17

FT CHAIN 18 144

FT FT GRANULOCYTE-MACROPHAGE COLONY-STIMULATING
 FT FACTOR.
 FT DISULFID 71 113
 FT DISULFID 105 138
 FT CARBOHYD 44 44
 FT CARBOHYD 54 54
 FT VARIANT 117 117
 FT TURN 25 27
 FT HELIX 30 44
 FT TURN 45 45
 FT HELIX 50 54
 FT STRAND 56 60
 FT HELIX 72 81
 FT TURN 82 82
 FT HELIX 85 103

FT TURN 104 104
 FT STRAND 115 119
 FT HELIX 120 131
 FT TURN 132 133
 SQ SEQUENCE 144 AA; 16295 MW; 112632 CN;

Query Match 99.4%; Score 1002; DB 2; Length 144;
 Best Local Similarity 95.1%; Pred. No. 4.08e-194;
 Matches 136; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

Db 1 mwlgsllllgtvacsisaparspsstqpwehvmaigearrlnlslrdaaemnetvevi 60
 |||||

Qy 1 mwlgsllllgtvacsisaparspsstqpwehvmaigearrlnlslrdaaemnetvev 60
 |||||

Db 61 semfdlqptclqtrlielykqglqsltklqpltmmaashyqhcpcptpetscatqitf 120
 |||||

Qy 61 semfdlqptclqtrlielykqglqsltklqpltmmaashyqhcpcptpetscatqitf 120
 |||||

Db 121 esfkenkdfllvipfdwepvq 143
 |||||

Qy 121 esfkenkdfllvipfdwepvq 143
 |||||

RESULT 2
 ID CSF2 SHEEP STANDARD; PRT; 144 AA.

AC P28773;

DT 01-DEC-1992 (REL. 24, CREATED)

DT 01-DEC-1992 (REL. 24, LAST SEQUENCE UPDATE)

DT 01-DEC-1992 (REL. 24, LAST ANNOTATION UPDATE)

DE GRANULOCYTE-MACROPHAGE COLONY-STIMULATING FACTOR PRECURSOR (GM-CSF)

DE (COLONY-STIMULATING FACTOR) (CSF).

OS OVIS ARIES (SHEEP).

OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;

OC EUTHERIA; ARTIODACTYLA.

RN [1]

RP SEQUENCE FROM N.A.

RM 92039044

RA MCINNES C.J., HAIG M.C.K.;

RL GENE 105:275-279 (1991).

CC -!- FUNCTION: GRANULOCYTE/MACROPHAGE COLONY-STIMULATING FACTORS ARE

CC CYTOKINES THAT ACT IN HEMATOPOIESIS BY CONTROLLING THE PRODUCTION,
 CC DIFFERENTIATION, AND FUNCTION OF 2 RELATED WHITE CELL POPULATIONS
 CC OF THE BLOOD, THE GRANULOCYTES AND THE MONOCYTES-MACROPHAGES.
 CC -!- FUNCTION: STIMULATES THE GROWTH AND DIFFERENTIATION OF

CC HEMATOPOIETIC PRECURSOR CELLS FROM VARIOUS LINEAGES, INCLUDING
 CC GRANULOCYTES, MACROPHAGES, EOSINOPHILS AND ERYTHROCYTES.
 CC -!- SUBUNIT: MONOMER.

DR EMBL; X53561; OOGMCSFR.

DR PIR; JH0469; JH0469.

DR HSSP; P04141; 1CSG.

DR PROSITE; PS00702; GM CSF.

KW CYTOKINE; GROWTH FACTOR; GLYCOPROTEIN; SIGNAL.

FT SIGNAL 1 17

FT CHAIN 18 144

FT FT GRANULOCYTE-MACROPHAGE COLONY-STIMULATING
 FT FACTOR.
 FT DISULFID 71 113
 FT DISULFID 105 138
 FT CARBOHYD 44 44
 FT POTENTIAL.
 SQ SEQUENCE 144 AA; 16318 MW; 117795 CN;

Query Match 82.1%; Score 828; DB 2; Length 144;
 Best Local Similarity 77.6%; Pred. No. 1.21e-154;
 Matches 111; Conservative 10; Mismatches 22; Indels 0; Gaps 0;

Db	1	mwlqnl1lllgtwvcsfsaptrqpsvtrpqwhvdaklealslndscdtaavmdetv	60
		: : : : : : : : :	
Qy	1	mwlqnl1lllgtvacsiqpspxspqgwehvnaiqearllnlsrdtaeknetv	60
		: : : : : : : :	
Db	61	semfdsqptcltrlelykgilrgsltaltsltnmaahykhkcpcptqaceti	120
		: : : : : : : :	
Qy	61	semfdlqptcltrlelykgilrgsltaltsltnmaahykhkcpcptscatq	120
		: : : : : : : :	
Db	121	kfskenlkdfliipfdwepvq	143
		: : : : : : : :	
Qy	121	esfkenlkdfliixpfdwepvq	143
		: : : : : : : :	

[illegible]

Query Match	76.7%;	Score 773;	DB 2;	Length 143;
Best Local Similarity	69.2%;	Pred. No. 3,01e-142;		
Matches	99;	Conservative 20;	Mismatches 12;	Indels 1; Gaps 1;
Db	1	mwlgqlllllgtwcfscfsaprrptnatrpgwhdkaikalsllhssdt	davmndt-	evv 59
Qy	1	mwlgslllllgtvacssapxspkspgwhvnaigearlllslrdaaenxetvev	60	

Db	60	sekfdsepcclqrklkyknglqgsaltelmgsltmashyehkcpptetsecqtqfief	119
QY	61	semfdlgepcclqrlelykqglqgsrlklkpgltmashyehkcpptetsecatqxif	120
Db	120	kfkedlkeflfiipdcwepaq	142
QY	121	esfkenlkdfllvxpfdcwepvq	143

RESULT	4
ID	CSF2 MOUSE STANDARD; PRT; 141 AA.
AC	P01587;
DT	21-JUL-1986 (REL. 01, CREATED)
DT	01-APR-1988 (REL. 07, LAST SEQUENCE UPDATE)
DT	01-AUG-1992 (REL. 23, LAST ANNOTATION UPDATE)
DE	GRANULOCYTE-MACROPHAGE COLONY-STIMULATING FACTOR PRECURSOR (GM-CSF)
DE	(COLONY-STIMULATING FACTOR) (CSF).
OS	MUS MUSCULUS (MOUSE).
OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC	EUTHERIA; RODENTIA.
[1]	RN RN SEQUENCE FROM N.A.
RM	86030234
RA	MIYATAKE S., OTSUKA T., YOKOTA T., LEE F., ARAI K.;
RL	EMBO J. 4:2561-2568(1985).
[2]	RN RN SEQUENCE FROM N.A.
RM	86030235
RA	STANLEY E.R., METCALF D., SOBIESZCZUK P., COUGH N.M., DUNN A.R.;
RL	EMBO J. 4:2569-2573(1985).
[3]	RN RN SEQUENCE FROM N.A.
RM	86030236
RA	DE LAMARTER J.F., MERMOD J.-J., LIANG C.M., ELIASON J.F.,
RA	THATCHER D.R.;
RL	EMBO J. 4:2575-2581(1985).
[4]	RN RN SEQUENCE FROM N.A.
RC	STRAIN-BALB/C;
RM	85230531
RA	GOUGH N.M., METCALF D., GOUGH J., GRAIL D., DUNN A.R.;
RL	EMBO J. 4:645-653(1985).
[5]	RN RN SEQUENCE OF 24-141 FROM N.A.
RC	TISSUE=LUNG;
RM	84245825
RA	GOUGH N.M., GOUGH J., METCALF D., KELSO A., GRAIL D., NICOLA N.A.,
RA	BURGESS A.W., DUNN A.R.;
RL	NATURE 309:763-767(1984).
[6]	RN RN SEQUENCE OF 18-141 FROM N.A.
RM	85298329
RA	CANTRELL M.A., ANDERSON D., CERRETTI D.P., PRICE V., MCKERECHAN K.,
RA	TUSHINSKI R.J., MOCHIZUKI D.Y., LARSEN A., GRABSTEIN S., GILLIS S.,
RA	COSMAN D.;
RL	PROC. NATL. ACAD. SCI. U.S.A. 82:6250-6254(1985).
[7]	RN RN DISULFIDE BONDS.
RM	88076878
RA	SCHRIMSER J.L., ROSE K., SIMONA M.G., WINGFIELD P.;
RL	BIOCHEM. J. 247:195-199(1987).
[8]	RN RN MUTAGENESIS.
RM	91161633

[illegible][illegible]

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92 gpltmashykhqhcptpetscatxift--esfkenkd-flivxpfdcwepv 142
QY      |||| ::|| : : || || || : ||:: ||| :

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RESULT	7	STANDARD;	PRT;	667 AA.
ID	ENV GALV			
AC	P21415.			
DT	01-MAY-1991 (REL. 18, CREATED)			
DT	01-MAY-1991 (REL. 18, LAST SEQUENCE UPDATE)			
DT	01-MAY-1991 (REL. 18, LAST ANNOTATION UPDATE)			
DE	ENV POLYPROTEIN PRECURSOR (CONTAINS: KNOB PROTEIN GP70; SPIKE PROTEIN P15E).			
GN	ENV.			
OS	GIBBON APE LEUKEMIA VIRUS.			
OC	VIRULIDE; SS-RNA ENVELOPED VIRUSES; POSITIVE-STRAND; RETROVIRIDAE; ONCOVIRINAE.			
RP	SEQUENCE FROM N.A.			
RM	90051069			
RA	DELAUSSUS S., SONIGO P., MAIN-HOBSON S.;			
RL	VIRIOLOGY 173:205-213(1989).			
DR	EMBL; M26927; PCCGPE. PIR; C32595; VCLIGL.			
KM	COAT PROTEIN; GLYCOPROTEIN; POLYPROTEIN; TRANSMEMBRANE; SIGNAL.			
FT	SIGNAL	1	42	
FT	CHAIN	43	489	KNOB PROTEIN GP70.
FT	CHAIN	490	667	SPIKE PROTEIN P15E.
FT	TRANSMEM	492	508	POTENTIAL.
FT	TRANSMEM	637	653	POTENTIAL.
FT	CARBOHYD	301	301	POTENTIAL.
FT	CARBOHYD	344	344	POTENTIAL.
FT	CARBOHYD	415	415	POTENTIAL.
FT	CARBOHYD	421	421	POTENTIAL.
FT	CARBOHYD	433	433	POTENTIAL.
FT	CARBOHYD	453	453	POTENTIAL.
SO	SEQUENCE	667 AA;	73729 MW;	2334159 CN;
Query Match		9.0%;	Score 91;	DB 3;
Best Local Similarity		29.3%;	Pred. No. 5.67e-01;	
Matches	17;	Conservative	16;	Mismatches 23;
				Indels 2;
				Gaps 2;
Db	499	lllgltagtgigqstaltkqpi-dlqgqlslqlaladlralqdvskledstls	555	
Oy	42	llhslrdaaeetvexseamdqpe-tclqtreltlykqglqsltklptmma	98	
RESULT	8			
ID	ACH1 DROME	STANDARD;	PRT;	567 AA.
AC	P09478;			
DT	01-MAR-1989 (REL. 10, CREATED)			
DT	01-MAR-1989 (REL. 10, LAST SEQUENCE UPDATE)			
DT	01-FEB-1994 (REL. 28, LAST ANNOTATION UPDATE)			
DE	ACETYLCHOLINE RECEPTOR PROTEIN, ALPHA-LIKE CHAIN 1 PRECURSOR.			
GN	ACHR OR ALS OR ACR96AA.			
OS	DROSOPHILA MELANOGASTER (FRUIT FLY).			
OC	EUKARYOTA; METAZOA; ARTHROPODA; INSECTA; DIPTERA.			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=OREGON-R;			
RA	88283626			
RA	BOSSY B., BALIVET M., SPIERER P.;			
RL	EMBO J. 7:611-618(1988).			
CC	-I- FUNCTION: AFTER BINDING ACETYLCHOLINE, THE ACHR RESPONDS BY AN			
CC	EXTENSIVE CHANGE IN CONFORMATION THAT AFFECTS ALL SUBUNITS AND			

CC LEADS TO OPENING OF AN ION-CONDUCTING CHANNEL ACROSS THE PLASMA
CC MEMBRANE.

CC	-1	DEVELOPMENTAL STAGE: LATE EMBRYONIC, LATE PUPAL AND SECOND INSTAR
CC	CC	LARVAE STAGES.
CC	-1	SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC	-1	SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNELS FAMILY.
DR	EMBL, X07194;	DNALSR.
DR	PIR, S00381;	ACEPAL.
DR	FLYBASE; FBGN0000036;	ACR96AA.
DR	PROSITE; PS00236;	NEUROR_ION CHANNEL.
KM	RECEPTOR; POSTSYNAPTIC MEMBRANE; IONIC CHANNEL; GLYCOPROTEIN; SIGNAL;	TRANSMEMBRANE; MULTIGENE FAMILY.
FT	SIGNAL	1 21
FT	CHAIN	22 567
FT	DOMAIN	22 240
FT	TRANSMEM	241 264
FT	TRANSMEM	272 290
FT	TRANSMEM	306 325
FT	DOMAIN	326 513
FT	TRANSMEM	514 532
FT	DISULFID	149 163
FT	DISULFID	222 223
FT	CARBOHYD	45 45
FT	CARBOHYD	233 233
FT	VARIANT	538 538
SC	SEQUENCE	567 AA; 64016 MW; 1720346 CN;
Query Match 8.9%; Score 90; DB 1; Length 567;		
Best Local Similarity 27.5%; Pred. No. 7.69e-01;		
Matches 19; Conservative 17; Mismatches 29; Indels 4; Gaps 4;		
Db	311	emb vtlsavntla-vlhmfsfpythmawqgflfiqlpklclcielpkkeepeedqpp 369
Qy	1	mmlqslallqgtacsiapxrsrp-spaxqgmehnaigearllnlsr-dta-aexneiv 57
Db	370	evlcvdyhl 378
Qy	58	evxseamfdl 66
RESULT 9		
ID	APE RAT	STANDARD; PRT; 311 AA.
AC	P02650;	
DT	21-JUL-1986 (REL. 01, CREATED)	
DT	13-AUG-1987 (REL. 05, LAST SEQUENCE UPDATE)	
DT	01-FEB-1994 (REL. 28, LAST ANNOTATION UPDATE)	
DE	APOLIPOPROTEIN E PRECURSOR (APO-E).	
CN	APOE.	
OS	RATTUS NORVEGICUS (RAT).	
OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;	
OC	EUTHERIA; RODENTIA.	
NC	(1)	
RM	SEQUENCE FROM N.A.	
RM	87091580	
RA	FUKAZAWA C., MATSUMOTO A., TAYLOR L.M.;	
RL	NUCLEIC ACIDS RES. 14:9527-9528 (1986).	
LN	(2)	
RP	SEQUENCE FROM N.A.	
RM	871008617	
RA	FUNG W.-P., HOWLETT G.J., SCHREIBER G.;	
RL	J. BIOL. CHEM. 261:13777-13783 (1986).	
LN	(3)	

RP	SEQUENCE FROM N.A.
RM	83238546
RA	MCLEAN J.M., FUKAZAWA C., TAYLOR J.M.;
RL	J. BIOL. CHEM. 258:8993-9000(1983).
CC	-I- FUNCTION: APO-E MEDIATES BINDING, INTERNALIZATION, AND CATABOLISM OF LIPOPROTEIN PARTICLES. IT CAN SERVE AS A LIGAND FOR THE LDL(APO B/E) RECEPTOR AND FOR THE SPECIFIC APO-E RECEPTOR (CHYLOMICRON REMNANT) OF HEPATIC TISSUES.
CC	-I- SUBCELLULAR LOCATION: EXTRACELLULAR.
CC	-I- THE MATURE PROTEIN HAS NO CYSTEINE RESIDUES; HOWEVER, IN DIFFERENT ALLELIC VARIANTS WHERE CYSTEINE RESIDUES REPLACE ANGININE AT POSITIONS 155 OR 168, BINDING OF APO-E TO CELL MEMBRANE RECEPTORS IS DECREASED. THE AMINO END OF THIS PROTEIN IS THEREFORE THOUGHT TO INTERACT WITH THE RECEPTOR.
DR	EMBL; X04979; RNAPOEC.
DR	EMBL; J02582; RNAPOEA.
DR	PIR; A03094; LPRE-
DR	PIR; A25576; A25576.
DR	PIR; A26189; A26189.
DR	HSSP; P02649; ILE4.
KM	GLYCOPROTEIN; PLASMA, LIPID TRANSPORT; HDL; VLDL; CHYLOMICRON;
KM	SIALIC ACID; HEPARIN-BINDING; REPEAT; SIGNAL.
FT	SIGNAL 1 18
FT	CHAIN 19 311
FT	DOMAIN 154 157
FT	DOMAIN 220 227
FT	DOMAIN 72 246
FT	REPEAT 72 93
FT	REPEAT 94 115
FT	REPEAT 116 137
FT	REPEAT 138 159
FT	REPEAT 160 181
FT	REPEAT 182 203
FT	REPEAT 204 224
FT	REPEAT 225 246
FT	CONFLICT 104 104
FT	CONFLICT 110 110
FT	CONFLICT 141 141
FT	CONFLICT 308 309
FT	CONFLICT 206 212
EQ	SEQUENCE 311 AA; 36038 MW; 419056 CN;
Query Match	8.8%; Score 89; DB 1; Length 311;
Best Local Similarity	30.4%; Pred. No. 1.04e+00;
Matches 28; Conservative	19; Mismatches 37; Indels 8; Gaps 8;
Dh	4 lwalllyplltcclaageleevtdqjpygsddpmegalnrfwvjlyrwvqls-dqvgeelq 62 : : : : : : : : : : : : : : : : : : : : Qy 1 mwlgsl--ll-gtva-csisapxrpsspxkqneh-vnaige-arlllnlsrdaaeane 55
Dh	63 ssqvtglvlmedt-m-fevakaykkeleeq 92 : : : : : : : : : : : : : : : : : : : : Qy 56 tvevxsemdlqepctclqtlllelykqqlgsl 87
RESULT 10	
ID AKIH ECOLI STANDARD; PRT; 820 AA.	
AC P00561;	
DT 21-JUL-1986 (REL. 01, CREATED)	
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)	
DT 01-FEB-1995 (REL. 31, FAST ANNOTATION UPDATE)	
DE ASPAROKINASE I (EC 2.7.2.4) / HOMOSERINE DEHYDROGENASE I (EC 1.1.1.3).	
EN THR1 (THR1); THR2).	

OS	ESCHERICHIA COLI.
OC	PROKARYOTA, GRACILICUTES, SCOTOBACTERIA, FACULTATIVELY ANAEROBIC RODS,
OC	ENTEROBACTERIACEAE.
CC	(1)
RP	SEQUENCE FROM N.A.
RM	810717247
RA	KATINKA M., COSSART P., SIBILLI L., SAINT-GIRONS I., CHALVIGNAC M.A.,
RA	LE BRAS G., COHEN G.N., YANIV M.;
RL	PROC. NATL. ACAD. SCI. U.S.A. 77:5730-5733(1980).
RM	(12)
RP	SEQUENCE FROM N.A.
RC	STRAIN=K12;
RM	92334977
RA	YURA T., MORI H., NAGAI H., NAGATA T., ISHIIHAMA A., FUJITA N.,
RA	ISONO K., MIZOBUCHI K., NAKATA A.;
RL	NUCLEIC ACIDS RES. 20:3305-3308(1992).
RP	(13)
RP	SEQUENCE FROM N.A.
RC	STRAIN=K12 / MG1655;
RC	BURLAND V.D., PLUNKETT G. III, BLATTNER F.R.;
RL	SUBMITTED (AUG-1994) TO EMBL/GENBANK/DBJ DATA BANKS.
RM	(14)
RP	SEQUENCE OF 51-129.
RM	800433179
RA	SIBILLI L., LE BRAS G., COSSART P., CHALVIGNAC M.A., LE BRAS G.,
RA	BRILEY P.A., COHEN G.N.;
RL	BIOCHIMIE 61:733-739(1979).
RM	(15)
RP	REVISION TO 11.
RM	83135751
RA	COSSART P.;
RL	UNPUBLISHED RESULTS, CITED BY:
RL	ZAKIN M.M., DUCHANE N., FERRARA P., COHEN G.N.;
RL	J. BIOL. CHEM. 258:3028-3031(1983).
CC	-1- PATHWAY: CATALYZES 2 NONCONSECUTIVE REACTIONS IN THE COMMON
CC	BIOSYNTHETIC PATHWAY LEADING FROM ASP TO DIAMINOPIMELATE AND LYS,
CC	TO MET. AND TO THR AND ILE.
CC	-1- CATALYTIC ACTIVITY: L-HOMOSERINE + NAD(P) (+) = L-ASPARATE
CC	BETA-SEMIALDEHYDE + NAD(P) H.
CC	-1- CATALYTIC ACTIVITY: ATP + L-ASPARTATE = ADP + 4-PHOSHO-L-
CC	ASPARTATE.
CC	-1- SUBUNIT: HOMOTETRAMER.
CC	-1- ENZYME REGULATION: THE ENZYME ACTIVITIES ARE REGULATED
CC	ALLOSTERICALLY BY L-THREONINE.
CC	-1- ASPARTOKINASE II-HOMOSERINE DEHYDROGENASE II AND ASPARTOKINASE
CC	III ALSO CATALYZE THE SAME REACTION(S).
CC	-1- SIMILARITY: TO OTHER ASPARTOKINASES AND HOMOSERINE DEHYDROGENASES
DR	EMBL; J01361; ECTHRA.
DR	EMBL; J01706; ECTHR.
DR	EMBL; X68872; ECTHREPO.
DR	EMBL; D10483; ECPAH02.
DR	EMBL; U14003; ECDW93.
DR	PIR; A00671; DECK.
DR	PIR; S40531; S40531.
DR	ECOGENE; EGI0998; THRA.
DR	PROSITE; PS00324; ASPARTOKINASE.
KM	TRANSFERASE, KINASE, OXIDOREDUCTASE, THREONINE BIOSYNTHESIS, NADP;
KM	ALLOSTERIC ENZYME, MULTIFUNCTIONAL ENZYME.
FT	DOMAIN 1 249 ASPARTOKINASE I.
FT	DOMAIN 250 470 INTERFACE.
FT	DOMAIN 471 820 HOMOSERINE DEHYDROGENASE I.
FT	NP BIND 471 478 NADP (POTENTIAL).
FT	CONFLICT 113 113 Q -> E (IN REF. 4).
FT	CONFLICT 230 230 N -> D (IN REF. 3).

WAPSEH

(TW)

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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Fri Jun 21 12:20:01 1996; MasPar time 5.44 Seconds
219,061 Million cell updates/sec

Tabular output not generated.

Title: >P60535
Description: (1-144) from p60535.pap
Perfect Score: 1008
Sequence: 1 mwlgalllgtvacsisapx.....enlkdfllvxpfdwepvqx 144

Scoring table: PAM 150
Gap 11

Searched: 70887 seqs, 8282111 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: a-geneseq2
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14

Statistics: Mean 30.234; Variance 133.218; scale 0.227

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	Query %	Match	Length	ID	Description	Pred. No.
1	1008	100.0	144	2	P81886		Sequence of human gra	3.92e-84
2	1008	100.0	144	3	P60535		Colony stimulating fa	3.92e-84
3	1002	99.4	144	13	R71118		GM-CSF encoded by clo	1.48e-83
4	1002	99.4	144	3	P60418		Human granulocyte mac	1.48e-83
5	1002	99.4	144	2	P70657		Sequence of a human g	1.48e-83
6	1002	99.4	144	1	R04098		Metaprotease gen	1.48e-83
7	1002	99.4	144	2	P81885		Sequence of human gra	1.48e-83
8	993	98.5	144	1	P80527		Granulocyte macrophag	1.08e-82
9	993	98.5	144	2	P70656		Sequence of a human g	1.08e-82
10	976	96.8	142	2	P94855		Human granulocyte mac	4.63e-81
11	899	89.2	131	2	P70351		Sequence of granulocy	1.11e-73
12	895	88.8	131	3	P60350		Human granulocyte mac	2.69e-73

13	871	86.4	127	8	R41540	r-h-GM-CSF.	5.33e-71
14	871	86.4	127	3	R13215	Oxidised GM-CSF.	5.33e-71
15	871	86.4	127	7	R33774	Recombinant human Gra	5.33e-71
16	871	86.4	128	1	P90118	Synthetic human granu	5.33e-71
17	871	86.4	128	1	P90115	Synthetic human granu	5.33e-71
18	864	85.7	127	14	R72357	Human granulocyte mac	2.49e-70
19	864	85.7	127	1	P91061	Human granulocyte-mac	2.49e-70
20	864	85.7	127	1	P91890	Amino acid sequence o	2.49e-70
21	862	85.5	128	1	R03199	New human granular ma	3.87e-70
22	861	85.4	128	1	R81001	Sequence (I) of human	4.82e-70
23	860	85.3	127	2	R08268	Crystalline recombinan	6.00e-70
24	857	85.0	127	7	R33775	Human Leu23-GM-CSF mu	1.16e-69
25	857	85.0	132	2	P70363	Sequence of human gra	1.16e-69
26	848	84.1	275	5	R26360	PIXY 344.	8.43e-69
27	848	84.1	275	3	R20114	Human IL-3/GM-CSF fus	8.43e-69
28	848	84.1	275	2	R11067	IL-3/GM-CSF fusion pr	8.43e-69
29	848	84.1	275	4	R23852	IL-3/GM-CSF fusion pr	8.43e-69
30	841	83.4	133	14	R72358	Human granulocyte mac	3.93e-68
31	841	83.4	271	2	R11066	GM-CSF/IL-3 fusion pr	3.93e-68
32	841	83.4	271	4	R23851	GM-CSF/IL-3 fusion pr	3.93e-68
33	841	83.4	271	3	R20113	Human GM-CSF/IL-3 fus	3.93e-68
34	841	83.4	271	5	R26359	PIXY 321.	3.93e-68
35	835	82.8	131	2	P70364	Sequence of human gra	1.47e-67
36	826	81.9	133	3	R13164	hGM-CSF[Leu23Asp27Glu	1.07e-66
37	821	81.4	144	4	R23662	Ovine GM-CSF.	3.20e-66
38	771	76.5	143	2	P94870	Sequence of bovine gr	1.88e-61
39	767	76.1	144	10	R54818	CHEF-2.	4.52e-61
40	752	74.6	144	5	R25699	CaGM-CSF.	1.21e-59
41	418	41.5	118	3	P50294	Sequence of mammalian	3.32e-28
42	416	41.3	118	2	R07611	Murine granulocyte-ma	5.09e-28
43	172	17.1	23	2	R10325	Granulocyte macrophag	3.54e-06
44	153	15.2	27	1	P91151	Wild-type human granu	1.36e-04
45	143	14.2	20	2	P70733	Sequence of leader po	8.96e-04

ALIGNMENTS

RESULT 1
ID P81886 standard; protein; 144 AA.
AC P81886;
DT 29-DEC-1990 (first entry)
DE Sequence of human granulocyte macrophage colony stimulating factor
DE (GM-CSF)
KW Lymphokine; interleukin-3; cancer therapy.
OS Homo sapiens.
FH Key Location/Qualifiers
FT Peptide 1..17
FT Protein 18..144
FT Region 44..46
FT /note="Region R1"
FT Region 54..56
FT /note="Region R2"
FN W08805786-A.
PD 11-AUG-1988.
PF 05-FEB-1988; U00335.
PR 06-FEB-1987; US-011794.
PA (GENE-) Genetics Inst.
PI Clark SC, Wong GG, Donahue RE;
DR WPI; 88-235149/33.
DR N-PSDB; N82363.
PT Colony stimulating factors having reduced carbohydrate levels -
PT obtd. by replacing and/or deleting asparagine residues in GM-CSF
PT sequences
PS Disclosure; Table 1, Page 6; 32pp; English.

CC Proteins characterised by possessing GM-CSF-type biological activity
 CC and having specified peptide sequence, except that 1-6 AAs are replaced
 CC and/or deleted within regions Asn-27 - Ser-29 and Asn-37 - Thr-39, such
 CC that one or both of the regions are completely deleted or replaced by a
 CC single AA residue, a dipeptide or a tripeptide sequence other than
 CC Asn-X-Ser or Asn-X-Thr, where X = any AA except for Pro is claimed. Also
 CC claimed are cDNA encoding proteins. Variants are active CSFs which may
 CC be produced in more homogeneous form and which may possess improved
 CC pharmacokinetic profiles relative to natural or recombinant GM-CSF.
 SQ Sequence 144 AA;

Query Match 100.0%; Score 1008; DB 2; Length 144;
 Best Local Similarity 95.8%; Pred. No. 3.92e-84;
 Matches 137; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Db 1 mwqlslllgtvacsisaprspsrqpwehvnaiqearrllnlsrdtaaeinetvew 60
 |||||
 Qy 1 mwqlslllgtvacsisaprspsrqpwehvnaiqearrllnlsrdtaaeinetvew 60
 |||||

Db 61 semfdlqptclqtrlykqglqsltklqpltmashyqhcbptpescatqitf 120
 |||||
 Qy 61 semfdlqptclqtrlykqglqsltklqpltmashyqhcbptpescatqitf 120
 |||||

Db 121 esfkenlkdfllvtpfdwepvq 143
 |||||
 Qy 121 esfkenlkdfllvxpfcdwepvq 143
 |||||

RESULT 2

ID P60535 standard; Protein; 144 AA.

AC P60535;

DT 30-JUL-1991 (first entry)

DE Colony stimulating factor (CSF) variant.

KW Colony stimulating factor.

OS Homo sapiens.

FH Key Location/Qualifiers

FT Misc difference 20

FT /label= Ser in gibbon CSF

FT Misc difference 27

FT /label= Arg in gibbon CSF

FT Misc difference 53

FT /label= Ile in gibbon CSF

FT Misc difference 60

FT /label= Val in gibbon CSF

FT Misc difference 117

FT /label= Thr in human CSF-Thr

FT Misc difference 117

FT /label= Ile in human CSF-Ile

FT Misc difference 134

FT /label= Thr in gibbon CSF

FT Misc difference 143

FT /label= Gly in gibbon CSF

PN W08600639-A.

PD 30-JAN-1986.

PF 04-JUL-1985; E00326.

PR 06-JUL-1984; US-628342.

PR 19-SEP-1984; US-652742.

PR 19-SEP-1984; US-652447.

PA (SANO J) SANDOZ AG.

PI Clark SC, Kaufman RJ, Wong GG, Wang EA.

DR WPI; 86-042122/06.

DR N-PSDB; N60457.

PT Recombinant colony stimulating factor protein - used for treating infection or granulocytopenia or activating neutrophils in

PT animals.

PS Disclosure; Fig 1; 91pp; English.

CC The sequence are human CSF variants (CSF-Ile and CSF-Thr), and
 CC gibbon granulocyte-macrophage CSF. The CSFs are lymphokines used
 CC to treat myelosuppression, especially symptomatic
 CC granulocytopenia.
 SQ Sequence 144 AA;

Query Match 100.0%; Score 1008; DB 3; Length 144;
 Best Local Similarity 95.8%; Pred. No. 3.92e-84;
 Matches 137; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Db 1 mwqlslllgtvacsisaprspsrqpwehvnaiqearrllnlsrdtaaeinetvew 60
 |||||
 Qy 1 mwqlslllgtvacsisaprspsrqpwehvnaiqearrllnlsrdtaaeinetvew 60
 |||||

Db 61 semfdlqptclqtrlykqglqsltklqpltmashyqhcbptpescatqitf 120
 |||||
 Qy 61 semfdlqptclqtrlykqglqsltklqpltmashyqhcbptpescatqitf 120
 |||||

Db 121 esfkenlkdfllvtpfdwepvq 143
 |||||
 Qy 121 esfkenlkdfllvxpfcdwepvq 143
 |||||

RESULT 3

ID R71118 standard; Protein; 144 AA.

AC R71118;

DT 12-OCT-1995 (first entry)

DE GM-CSF encoded by clone pCD-human-GM-CSF cDNA insert.

KW Human; granulocyte-macrophage colony stimulating factor; GM-CSF;

KW E.coli; quaternary amino ethyl anion exchange chromatography;

KW red 120 triazinyl dye-ligand affinity chromatography;

KW gel filtration column chromatography; stimulation; blood cell.

OS Homo sapiens.

PN US5391706-A.

PD 21-FEB-1995.

PF 16-JUL-1987; 074410.

PR 16-JUL-1987; US-074410.

PR 15-DEC-1989; US-455453.

PR 14-APR-1992; US-870153.

PR 21-SEP-1993; US-125356.

PA (SCHE J) SCHERING-PLOUGH CORP.

PI Kosecki RA, Reichert P, Seelig GF, Trotta PP;

DR WPI; 95-098169/13.

DR N-PSDB; Q84865.

PT Purifying granulocyte-macrophage colony-stimulating factor - by
 PT anion-exchange, dye-ligand affinity, gel filtration and
 PT reversed-phase chromatography

PS Disclosure; Column 3-4; 5pp; English.

CC This sequence represents human granulocyte-macrophage colony stimulating
 CC factor (GM-CSF). Heterogeneity of the nucleotide sequence and the
 CC amino acid sequence has been observed and this sequence was deposited
 CC in E.coli as ATCC 39923. The GM-CSF protein was isolated using the
 CC method of the invention. The method comprises killing and disrupting
 CC GM-CSF-expressing bacteria and preparing a GM-CSF containing extract
 CC from the disrupted cells. This extract is subjected to quaternary amino
 CC ethyl (QAE) anion exchange chromatography to separate proteases and
 CC produce protease-free GM-CSF fractions. These fractions are subjected
 CC to red 120 triazinyl dye-ligand affinity chromatography to obtain
 CC GM-CSF containing fractions free of hydrophobic impurities. These
 CC fractions are then subjected to gel filtration column chromatography to
 CC produce GM-CSF containing fractions free of high and low mol. wt.
 CC impurities which are then subjected to reversed-phase column

CC chromatography to produce fractions with a purity of greater than 95%.
 CC The obtained GM-CSF may be used in clinical situations where the
 CC stimulation of blood cell generation is desirable.
 SQ Sequence 144 AA;

Query Match 99.4%; Score 1002; DB 13; Length 144;
 Best Local Similarity 95.1%; Pred. No. 1.48e-83;
 Matches 136; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

Db 1 mwlgsllllgtvacsisaparspsqpwehvnaigearrllnlsrdtaemnetvevi 60
 |||||
 Qy 1 mwlgsllllgtvacsisaparspsqpwehvnaigearrllnlsrdtaemnetvev 60
 |||||

Db 61 semfdlqptclqrlelykqglrsgtklkgpltmashyqhpcptpatscatqitf 120
 |||||
 Qy 61 semfdlqptclqrlelykqglrsgtklkgpltmashyqhpcptpatscatqitf 120
 |||||

Db 121 esfkenlkdfllvfpdcwepvq 143
 |||||
 Qy 121 esfkenlkdfllvfpdcwepvq 143
 |||||

RESULT 4

ID P60418 standard; protein; 144 AA.
 AC P60418;
 DT 01-JAN-1980 (first entry)
 DE Human granulocyte macrophage-colony stimulating factor.
 KW Granulocyte; macrophage; colony stimulating factor; chemotherap;
 KW Neoplastic disease therapy; infectious disease therapy; es.
 OS Homo sapiens.
 PN M08603225-A.
 PD 03-JUN-1986.
 PF 18-NOV-1985; U02250.
 PR 20-NOV-1984; US-673898.
 PA (SCHE) SCHERING BIOTECH CO.
 PI Yokota T, Lee FD, Rennick D, Arai K;
 DR WPI: 86-155831/24.
 DR N-PSDB; N60364.
 PT New polypeptide(s) for colony stimulation of granulocytes -
 PT useful for enhancing body defences against neoplasms and
 PT infectious diseases and to overcome myelo:suppression in
 PT chemotherapy
 PS Disclosure; Fig. 1; 53pp; English.
 CC The protein has GM-CSF activity and is useful in elucidating
 CC control mechanisms of mammalian immune responses. It is also
 CC useful for administration to enhance natural defences against
 CC neoplastic and infectious diseases or as an adjunct in chemotherapy
 CC to overcome myelosuppression. GM-CSF is prepared by conventional
 CC recombinant DNA techniques. The factor has activity on
 CC human neutrophilic granulocytes, macrophages and eosinophils.
 SQ Sequence 144 AA;

Query Match 99.4%; Score 1002; DB 3; Length 144;
 Best Local Similarity 95.1%; Pred. No. 1.48e-83;
 Matches 136; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

Db 1 mwlgsllllgtvacsisaparspsqpwehvnaigearrllnlsrdtaemnetvevi 60
 |||||
 Qy 1 mwlgsllllgtvacsisaparspsqpwehvnaigearrllnlsrdtaemnetvev 60
 |||||

Db 61 semfdlqptclqrlelykqglrsgtklkgpltmashyqhpcptpatscatqitf 120
 |||||
 Qy 61 semfdlqptclqrlelykqglrsgtklkgpltmashyqhpcptpatscatqitf 120
 |||||

Db 121 esfkenlkdfllvfpdcwepvq 143
 |||||
 Qy 121 esfkenlkdfllvfpdcwepvq 143
 |||||

RESULT 5

ID P70657 standard; Protein; 144 AA.
 AC P70657;
 DT 18-APR-1991 (first entry)
 DE Sequence of a human granulocyte-macrophage colony stimulating
 DE factor (hGM-CSF)-like polypeptide isolated from 5637 cell line.
 KW AIDS therapy; leukocyte; leucaemia.
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT Cleavage-site 17..18
 FT /note= "for signal peptide"
 PN M08702060-A.
 PD 09-APR-1987.
 PF 03-OCT-1986; U02106.
 PR 03-OCT-1985; US-783414.
 PA (BIOI) BIOGEN NV.
 PA (DELA) DELAMARTER J.
 PI Delamarter J, Ernst JF;
 DR WPI: 87-108701/15.
 DR N-PSDB; N71002.
 PT Human granulocyte-macrophage stimulating factor-like
 PT polypeptide(s) - produced from recombinant DNA sequence having 5'
 PT terminal alteration
 PS Example; Fig 2; 61pp; English.
 CC A recombinant DNA molecule encoding a hGM-CSF is claimed wherein
 CC there is a 5' terminal alteration allowing higher yield than the
 CC native DNA sequence. The cpds. may be used to reduce the
 CC likelihood of infections in immunologically
 CC compromised individuals, such as those suffering from AIDS by
 CC increasing their white blood cell count.
 SQ Sequence 144 AA;

Query Match 99.4%; Score 1002; DB 2; Length 144;
 Best Local Similarity 95.1%; Pred. No. 1.48e-83;
 Matches 136; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

Db 1 mwlgsllllgtvacsisaparspsqpwehvnaigearrllnlsrdtaemnetvevi 60
 |||||
 Qy 1 mwlgsllllgtvacsisaparspsqpwehvnaigearrllnlsrdtaemnetvev 60
 |||||

Db 61 semfdlqptclqrlelykqglrsgtklkgpltmashyqhpcptpatscatqitf 120
 |||||
 Qy 61 semfdlqptclqrlelykqglrsgtklkgpltmashyqhpcptpatscatqitf 120
 |||||

Db 121 esfkenlkdfllvfpdcwepvq 143
 |||||
 Qy 121 esfkenlkdfllvfpdcwepvq 143
 |||||

RESULT 6

ID R04098 standard; protein; 144 AA.
 AC R04098;
 DT 10-SEP-1990 (first entry)
 DE Metapyrocatechase gene product.
 KW Metapyrocatechase; GM-CSF; leukopaenia; osteomyelodysplasia;
 KW granulocyte macrophage colony stimulating factor; ds.
 OS Homo sapiens.
 PN J02076596-A.
 PD 15-MAR-1990.

08/466,308

PF 13-SEP-1988; 229468.
PR 13-SEP-1988; JP-229468.
PA (SAGA) Sagami Chem Res Centre.
DR WPI; 90-128250/17.
DR N-PSDB; Q04017.
PT Human granulocyte macrophage colony stimulating factor derivs. -
PT useful for treating diseases due to leukopenia or
PT osteomyelodysplasia.
PS Disclosure; P; Japanese.
CC Human GM-CSF derivs. have polypeptide fragment from N-terminal of
CC metapyrocatechase, bonded at its C-terminal to the N-terminal of
CC GM-CSF. Expression vectors pGM1 and pGM3 also contain the tac
CC promoter/operator and the SD sequence of metapyrocatechase.
SQ Sequence 144 AA;

Query Match 99.4%; Score 1002; DB 1; Length 144;
Best Local Similarity 95.1%; Pred. No. 1.48e-83;
Matches 136; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

Db 1 mwlgslilgtvacsisaparspsstqpwhehvnaigearrllnlsrdaaemnetvevi 60
|||||
Qy 1 mwlgslilgtvacsisaparspsstqpwhehvnaigearrllnlsrdaaemnetvevx 60
|||||

Db 61 semfdlqptclqrlelykqglqgsltklkgpltmashyqhpcptpetcatqitf 120
|||||
Qy 61 semfdlqptclqrlelykqglqgsltklkgpltmashyqhpcptpetcatqitf 120
|||||

Db 121 esfkenkdfllvfpdcwepvq 143
|||||
Qy 121 esfkenkdfllvfpdcwepvq 143
|||||

RESULT 7

ID P81885 standard; protein; 144 AA.
AC P81885;
DT 29-DEC-1990 (first entry)
DE Sequence of human granulocyte macrophage colony stimulating factor
DE (GM-CSF)
KW Lymphokine; interleukin-3; cancer therapy.
OS Homo sapiens.
FH Key Location/Qualifiers
FT Peptide 1..17
FT Protein 18..144
FT Region 44..46
FT /note="Region R1"
FT Region 54..56
FT /note="Region R2"
PN W08805786-A.
PD 11-AUG-1988.
PF 05-FEB-1988; U00335.
PR 06-FEB-1987; US-011794.
PA (GENE-) Genetics Inst.
PI Clark SC, Wong GG, Donahue RE;
DR WPI; 88-235149/33.
DR N-PSDB; N80223.
PT Colony stimulating factors having reduced carbohydrate levels -
PT obtd. by replacing and/or deleting asparagine residues in GM-CSF
PT sequences
PS Disclosure; Table 1, Page 6; 32pp; English.
CC Proteins characterised by possessing GM-CSF-type biological activity
CC having a specified peptide sequence, except that 1-6 AAs are replaced
CC and/or deleted within regions Asn-27 - Ser-29 and Asn-37 - Thr-39, such
CC that one or both of the regions are completely deleted or replaced by a
CC single AA residue, a dipeptide or a tripeptide sequence other than

CC Asn-X-Ser or Asn-X-Thr, where X = any AA except for Pro is claimed. Also
CC claimed are cDNA encoding proteins. Variants are active CSFs which may
CC be produced in more homogeneous form and which may possess improved
CC pharmacokinetic profiles relative to natural or recombinant GM-CSF.
SQ Sequence 144 AA;

Query Match 99.4%; Score 1002; DB 2; Length 144;
Best Local Similarity 95.1%; Pred. No. 1.48e-83;
Matches 136; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

Db 1 mwlgslilgtvacsisaparspsstqpwhehvnaigearrllnlsrdaaemnetvevi 60
|||||
Qy 1 mwlgslilgtvacsisaparspsstqpwhehvnaigearrllnlsrdaaemnetvevx 60
|||||

Db 61 semfdlqptclqrlelykqglqgsltklkgpltmashyqhpcptpetcatqitf 120
|||||
Qy 61 semfdlqptclqrlelykqglqgsltklkgpltmashyqhpcptpetcatqitf 120
|||||

Db 121 esfkenkdfllvfpdcwepvq 143
|||||
Qy 121 esfkenkdfllvfpdcwepvq 143
|||||

RESULT 8

ID P80527 standard; protein; 144 AA.
AC P80527;
DT 24-OCT-1990 (first entry)
DE Granulocyte macrophage colony stimulating factor.
DE Granulocyte macrophage colony stimulating factor;
KW cell line U937; ssDNA.
OS Homo sapiens.
FH Key Location/Qualifiers
FT /label=Ala
FT /note="N-terminal residue of mature hGM-CSF"
FT Misc-difference 97
FT /label=Ile
FT /note="differs from residue in hGM-CSF from Mo cells"
PN EP-281069-A.
PD 07-SEP-1988.
PF 01-MAR-1988; 103067.
PR 02-MAR-1987; JP-048580.
PA (SUMO) Sumitomo Pharm KK.
PI Nakayama C, Okamoto M, Yanagi H;
DR WPI; 88-251666/36.
DR N-PSDB; N81118.
PT Human granulocyte-macrophage colony stimulating factor
PT - produced in human cells transfected with exogenous
PT DNA encoding the factor.
PS Disclosure; P; English.
CC The sequence is that of human granulocyte macrophage colony
CC stimulating factor (hGM-CSF) derived from the human cell
CC line U937. The hGM-CSF is useful for the treatment of
CC infectious diseases or leukocytopenia which are caused by
CC e.g. irradiation therapy or chemotherapy. See also P80527.
SQ Sequence 144 AA;

Query Match 98.5%; Score 993; DB 1; Length 144;
Best Local Similarity 94.4%; Pred. No. 1.08e-82;
Matches 135; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Db 1 mwlgslilgtvacsisaparspsstqpwhehvnaigearrllnlsrdaaemnetvevi 60
|||||
Qy 1 mwlgslilgtvacsisaparspsstqpwhehvnaigearrllnlsrdaaemnetvevx 60
|||||

Db 61 semfdlqptclqrlelykqglqsgitklkqpltmashyqhgcptpsetcatqitf 120
 Qy 61 semfdlqptclqrlelykqglqsgitklkqpltmashyqhgcptpsetcatqitf 120

Db 121 esfkenlkdfllvfpdcwepvq 143
 Qy 121 esfkenlkdfllvfpdcwepvq 143

RESULT 9

ID P70656 standard; Protein; 144 AA.
 AC P70656;
 DT 18-APR-1991 (first entry)
 DE Sequence of a human granulocyte-macrophage colony stimulating
 DE factor (hGM-CSF)-like polypeptide isolated from U937 cell line.
 KW AIDS therapy; leukocyte; leucaemia.
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT Cleavage-site 17..18
 FT /note= "for signal peptide"
 FT Misc difference 116
 FT /label= Thr in Mo-cell deriv. cDNA
 PN W08702060-A.
 PD 09-APR-1987.
 PF 03-OCT-1986; U02106.
 PR 03-OCT-1985; US-783414.
 PA (BIOG) BIOGEN NV.
 PA (DELA/) DELAMARTER J.
 PI Delamarter J, Ernst JF;
 DR WPI; 87-108701/15.
 DR N-PSDB; N71001.
 PT Human granulocyte-macrophage stimulating factor-like
 PT polypeptide(s) - produced from recombinant DNA sequence having 5'
 PT terminal alteration
 PS Example; Fig 1; 61pp; English.
 CC A recombinant DNA molecule encoding a hGM-CSF is claimed wherein
 CC there is a 5' terminal alteration allowing higher yield than the
 CC native DNA sequence. The cpds. may be used to reduce the
 CC likelihood of infections in immunologically
 CC compromised individuals, such as those suffering from AIDS by
 CC increasing their white blood cell count.
 SQ Sequence 144 AA;

Query Match 98.5%; Score 993; DB 2; Length 144;
 Best Local Similarity 94.4%; Pred. No. 1.08e-82;
 Matches 135; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Db 1 mwlgslillgtvacsisaparspsqpwehvnaigearrllnlsrdaaemntevvi 60
 Qy 1 mwlgslillgtvacsisaparspsqpwehvnaigearrllnlsrdaaemntevv 60

Db 61 semfdlqptclqrlelykqglqsgitklkqpltmashyqhgcptpsetcatqitf 120
 Qy 61 semfdlqptclqrlelykqglqsgitklkqpltmashyqhgcptpsetcatqitf 120

Db 121 esfkenlkdfllvfpdcwepvq 143
 Qy 121 esfkenlkdfllvfpdcwepvq 143

RESULT 10

ID P94855 standard; protein; 142 AA.
 AC P94855;

DT 27-JUN-1989 (first entry)
 DE Human granulocyte macrophage colony stimulating factor polypeptide.
 KW Human granulocyte macrophage colony stimulating factor (GM-CSF);
 KW haematopoiesis; depressed blood cells.
 OS Homo sapiens.

FH Key Location/Qualifiers
 FT CDS 33..464
 FT polyA signal 780..787
 PN EP-299782-A.
 PD 18-JAN-1989.
 PF 15-JUL-1988; 306486.
 PR 17-JUL-1987; US-074988.
 PA (SCHE-) Schering Biotech. Co.
 PI Yokota T, Lee FD, Rennick DM, Arai K-I, Arai N.
 DR WPI; 89-017271/03.
 DR N-PSDB; N93172.
 PT Human granulocyte macrophage colony stimulating factor - used eg for
 PT haematopoiesis stimulation and used in treating depressed blood cell
 PT populations.
 PS Disclosure; fig.1; 40pp; English.

CC Corresponding cDNA sequence is inserted into an expression vector contg.
 CC eg SV40 origin, pref. also a bacterial origin, SV40 early- and SR alpha
 CC promoters, etc. The resulting library is screened and colonies selected
 CC which produce GM-CSF (i.e. those contg. plasmid pcD-human-GM-CSF). Modif-
 CC led forms of GM-CSF are made by producing mutant forms of cDNA esp. using
 CC cassette mutagenesis. These muteins can be glycosylated or non-glycosyl-
 CC ated, substd. (1-2 fold), deleted (1-fold) or inserted (1-fold) forms of
 CC GM-CSF. GM-CSF is useful in the treatment of myeloid hypoplasia and stim-
 CC ulates regeneration of the haematopoietic system following eg bone marrow
 CC transplants and some cancer treatments. Mutant forms show reduced side
 CC effects, improved stability towards proteases and increased yields.
 SQ Sequence 142 AA;

Query Match 96.8%; Score 976; DB 2; Length 142;
 Best Local Similarity 94.4%; Pred. No. 4.63e-81;
 Matches 135; Conservative 1; Mismatches 5; Indels 2; Gaps 1;

Db 1 mwlgslillgtvacsisaparspsqpwehvnaigearrllnlsrdaaemntevvi 58
 Qy 1 mwlgslillgtvacsisaparspsqpwehvnaigearrllnlsrdaaemntevv 60

Db 59 semfdlqptclqrlelykqglqsgitklkqpltmashyqhgcptpsetcatqitf 118
 Qy 61 semfdlqptclqrlelykqglqsgitklkqpltmashyqhgcptpsetcatqitf 120

Db 119 esfkenlkdfllvfpdcwepvq 141
 Qy 121 esfkenlkdfllvfpdcwepvq 143

RESULT 11

ID P70351 standard; Protein; 131 AA.

AC P70351;

DT 27-APR-1991 (first entry)

DE Sequence of granulocyte macrophage colony stimulating factor
 DE (GM-CSF) in plasmid pHG23.

KW Cancer therapy; tumoricide.

OS Homo sapiens.

FH Key Location/Qualifiers

FT Peptide 2..13

FT Protein 14..397

PN EP-211684-A.

PD 25-FEB-1987.

PF 15-AUG-1986; 306304.

Key	Location/Qualifiers
FT Protein	5..131
FT /label=mature protein	
PN EP-183350-A.	
PD 04-JUN-1986.	
PF 25-SEP-1985; 306827.	
PR 29-OCT-1984; US-666041.	
PR 02-JUL-1985; US-750401.	
PA (IMMU-) IMMUNEX CORP.	
PI Anderson DM, Cantrell MA, Cerretti DP, Cosman DJ, Larsen AD, ;	
PI Price VJ;	
DR WPI; 86-145553/23.	
PT New DNA encoding for expression of human colony stimulating	
PT factor - useful in prodn. of the factor, esp. granulocyte	
PT macrophage factor, for treating leukaemia and in bone marrow	
PT transplantation	
PS Disclosure; Fig. 2; 34pp; English.	
CC leukaemia; anaemia; bone marrow transplantation.	
CC Human granulocyte macrophage colony stimulating factor can be	
CC produced in large amts. In homogeneous form it is useful in the	
CC possible treatment of proliferative blood disorders, eg certain	

Db 1 aparspsstqpwheynaigearrlnlsrdtaemnetvevixsemfmldeptclqltrie 60
|| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 18 aprxpspxpwheynaigearrlnlsrdtaexnetvevxsefmldcptclqltrie 77

 W P S R E A
 (TW)

Release 2.1D John F. Collins, Biocomputing Research Unit.
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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Fri Jun 21 12:19:26 1996; MacPar time 6.88 Seconds
 528.733 Million cell updates/sec

Tabular output not generated.

Title: >p60535
 Description: (1-144) from p60535.rpr
 Perfect Score: 1008
 Sequence: 1 mwqlsllllgtvacsapx.....enlkdfllvxpfdwepvqx 144

Scoring table: PAM 150
 Gap 11

Searched: 82306 seqs, 25270970 residues

Post-processing: Minimum Match 0%
 Listing first 45 summaries

Database: pir46
 1:ann1 2:ann2 3:ann3 4:unann1 5:unann2 6:unann3 7:unann4
 8:unann5 9:unann6 10:unann7 11:unann8 12:unrev1
 13:unrev2

Statistics: Mean 41.316; Variance 95.998; scale 0.430

Pred. No. is the number of results predicted by chance to have a
 score greater than or equal to the score of the result being printed,
 and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	1002	99.4	144	2	FOHUGM granulocyte-macrophage	3.80e-153
2	828	82.1	144	5	JH0469 granulocyte-macrophage	5.21e-122
3	821	81.4	144	11	A61632 granulocyte-macrophage	9.19e-121
4	773	76.7	143	2	FOBOCM granulocyte-macrophage	3.14e-112
5	752	74.6	144	5	A44936 granulocyte-macrophage	1.67e-108
6	546	54.2	141	5	A24644 granulocyte-macrophage	2.53e-72
7	536	53.2	141	5	A24636 granulocyte-macrophage	1.37e-70
8	416	41.3	118	2	FQMSGM granulocyte-macrophage	5.37e-50
9	102	10.1	605	6	S33019 hypothetical protein	2.16e-01
10	102	10.1	605	3	QBEB29 BRILF1 protein - huma	2.16e-01
11	100	9.9	581	4	S50769 alpha-glucosidase ho	3.70e-01
12	97	9.6	146	10	D42402 cell surface glycopr	8.21e-01

13	93	9.2	90	8	S49112	hypothetical protein	2.33e+00
14	91	9.0	553	5	A42499	mullerian inhibiting	3.87e+00
15	91	9.0	667	3	VCLJGL	env polypeptide prec	3.87e+00
16	90	8.9	567	2	ACFFAL	nicotinic acetylchol	4.98e+00
17	89	8.8	311	5	A25576	apolipoprotein E pre	6.40e+00
18	89	8.8	311	2	LPRT	apolipoprotein E pre	6.40e+00
19	89	8.8	312	5	A26189	apolipoprotein E pre	6.40e+00
20	89	8.8	820	1	DEECK	thrA bifunctional en	6.40e+00
21	88	8.7	133	5	JC2202	secretin - mouse	8.21e+00
22	88	8.7	200	2	UNRTCF	ciliary neurotrophic	8.21e+00
23	87	8.6	514	4	S21125	steroid 17alpha-mono	1.05e+01
24	87	8.6	576	12	S01965	DNA-directed DNA pol	1.05e+01
25	87	8.6	865	9	A53186	fluG protein - Emeri	1.05e+01
26	87	8.6	2201	10	A54774	ATP binding cassette	1.05e+01
27	86	8.5	465	13	S20435	neurokinin-3 recepto	1.34e+01
28	86	8.5	500	10	S46328	intermediate filamen	1.34e+01
29	86	8.5	585	3	W2BE26	gene 26 protein - hu	1.34e+01
30	86	8.5	638	7	C64156	hypothetical protein	1.34e+01
31	86	8.5	815	7	A64048	aspartokinase-homose	1.34e+01
32	85	8.4	76	9	S37191	hypothetical protein	1.71e+01
33	85	8.4	199	2	B38285	interleukin-11 precu	1.71e+01
34	85	8.4	403	10	S41708	cyclin B3 - chicken	1.71e+01
35	85	8.4	417	7	C32185	Frz CD protein - Myx	1.71e+01
36	85	8.4	1403	10	S24548	homeotic protein pro	1.71e+01
37	85	8.4	1403	10	J01397	pros protein - fruit	1.71e+01
38	85	8.4	1407	10	A41089	neuronal precursor p	1.71e+01
39	85	8.4	1951	5	S18253	laminin chain A - fr	1.71e+01
40	85	8.4	3712	13	S28399	laminin chain A - fr	1.71e+01
41	84	8.3	304	10	S44801	FI0E9.2 protein - Ca	2.17e+01
42	84	8.3	418	10	A53120	intracellular coagul	2.17e+01
43	84	8.3	555	13	S20100	Mullerian inhibiting	2.17e+01
44	84	8.3	2429	2	SJH0A	spectrin alpha chain	2.17e+01
45	83	8.2	311	5	JU0036	apolipoprotein E pre	2.76e+01

ALIGNMENTS

RESULT	1
ENTRY	granulocyte-macrophage colony-stimulating factor precursor - human
TITLE	FOHUGM #type complete
ALTERNATE_NAMES	colony-stimulating factor 2; GM-CSF
ORGANISM	#formal name Homo sapiens #common name man
DATE	04-Dec-1986 #sequence_revision 04-Dec-1986 #text_change 18-Aug-1995
ACCESSIONS	C24636; A25169; A01853; A44175; JC1090
REFERENCE	A91015
#authors	Miyatake, S.; Otsuka, T.; Yokota, T.; Lee, F.; Arai, K.
#journal	EMBO J. (1985) 4:2561-2568
#title	Structure of the chromosomal gene for granulocyte-macrophage colony stimulating factor: comparison of the mouse and human genes.
#cross-references	MUID:86030234
#accession	C24636
#molecule type	DNA
#residues	1-144 #label MIY
#cross-references	EMBL:X03021
REFERENCE	A25169
#authors	Cantrell, M.A.; Anderson, D.; Cerretti, D.P.; Price, V.; McKereghan, K.; Tushinski, R.J.; Mochizuki, D.Y.; Larsen, A.; Grabstein, K.; Gillis, S.; Cosman, D.
#journal	Proc. Natl. Acad. Sci. U.S.A. (1985) 82:6250-6254
#title	Cloning, sequence, and expression of a human granulocyte/macrophage colony-stimulating factor.


```

#cross-references M01D:85298329
#accession A25169
##molecule_type mRNA
##residues 1-144 ##label CAN
##cross-references GB:M11734
REFERENCE
#authors Lee, F.; Yokota, T.; Otsuka, T.; Gemmell, L.; Larson, N.;
Luh, J.; Arai, K.; Rennick, D.
#journal Proc. Natl. Acad. Sci. U.S.A. (1985) 82:4360-4364
#title Isolation of cDNA for a human granulocyte-macrophage
colony-stimulating factor by functional expression in
mammalian cells.
#cross-references M01D:85242684
#accession A01853
##molecule_type mRNA
##residues 1-144 ##label LEE
##cross-references GB:M11220
REFERENCE
#authors Wong, G.G.; Witek, J.S.; Temple, P.A.; Wilkens, K.M.; Leary,
A.C.; Luxenberg, D.P.; Jones, S.S.; Brown, E.L.; Kay, R.M.;
Orr, E.C.; Shoemaker, C.; Golde, D.W.; Kaufman, R.J.;
Hewick, R.M.; Wang, E.A.; Clark, S.C.
#journal Science (1985) 228:810-815
#title Human GM-CSF: molecular cloning of the complementary DNA and
purification of the natural and recombinant proteins.
#accession A44175
##molecule_type mRNA
##residues 1-116, 'T', 118-144 ##label WON
##cross-references GB:M10663
##note parts of this sequence, including the amino end of the
mature protein, were confirmed by peptide sequencing
REFERENCE
#authors Wen, D.Y.; Huang, B.R.; Cai, L.W.; Si, J.Y.
#journal Acta Biochim. Biophys. Sin. (1993) 25:651-655
#title Amplification of human granulocyte-macrophage
colony-stimulating factor cDNA with the method of reverse
transcript-polymerase chain reaction.
#accession JCI090
##status preliminary
##molecule_type protein
##residues 18-21, 'C', 23-96, 'L', 98-144 ##label WEN
GENETICS
#gene GDB:CSF2
#map_position 5q23-q31
#introns 53/3; 67/3; 109/3
FUNCTION
#description stimulates the differentiation and proliferation of
hematopoietic progenitor cells into granulocytes,
macrophages, and perhaps eosinophils
CLASSIFICATION #superfamily granulocyte-macrophage colony-stimulating factor
KEYWORDS cytokine; glycoprotein; growth factor; macrophage; monomer;
T-cell
FEATURE
1-17 #domain signal sequence #status predicted #label SIG\
18-144 #product granulocyte-macrophage colony-stimulating
factor #status experimental #label MAT\
44,54 #binding_site carbohydrate (Asn) (covalent) #status
predicted
SUMMARY #length 144 #molecular-weight 16295 #checksum 8567
Query Match 99.4%; Score 1002; DB 2; Length 144;
Best Local Similarity 95.1%; Pred. No. 3.80e-153;
Matches 136; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

```

```

Db 1 mwlgslillgtvacsisaprspsqpwelhmaiqearllnlsrdtaamnetvev 60
|||||
Qy 1 mwlgslillgtvacsisaprspsqpwelhmaiqearllnlsrdtaamnetvev 60
|||||
Db 61 semfdlqepctcltrlelykqglrsgitklkplmtmashyqhpcptpsetcatqitf 120
|||||
Qy 61 semfdlqepctcltrlelykqglrsgitklkplmtmashyqhpcptpsetcatqitf 120
|||||
Db 121 esfkenlkdfllvxfdcwepvq 143
|||||
Qy 121 esfkenlkdfllvxfdcwepvq 143
|||||
RESULT 2
ENTRY JH0469 #type complete
TITLE granulocyte-macrophage colony-stimulating factor precursor -
sheep
ALTERNATE_NAMES colony-stimulating factor 2; GM-CSF
ORGANISM #formal_name Ovis orientalis aries, Ovis ammon aries
#common_name domestic sheep
DATE 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change
18-Jun-1993
ACCESSIONS JH0469; S16730
REFERENCE JH0469
#authors McInnes, C.J.; Haig, D.M.
#journal Gene (1991) 105:275-279
#title Cloning and expression of a cDNA encoding ovine
granulocyte-macrophage colony-stimulating factor.
#cross-references M01D:92039044
#accession JH0469
##molecule_type mRNA
##residues 1-144 ##label MCI
##cross-references GB:X53561
COMMENT This protein is a glycoprotein cytokine produced and secreted by
various cell types including activated T-cells and macrophages.
CLASSIFICATION #superfamily granulocyte-macrophage colony-stimulating factor
KEYWORDS cytokine; glycoprotein; growth factor; macrophage; monomer;
T-cell
FEATURE
1-17 #domain signal sequence #status predicted #label SIG\
18-144 #product granulocyte-macrophage colony-stimulating
factor #status predicted #label MAT\
44 #binding_site carbohydrate (Asn) (covalent) #status
predicted
SUMMARY #length 144 #molecular-weight 16318 #checksum 9541
Query Match 82.1%; Score 828; DB 5; Length 144;
Best Local Similarity 77.6%; Pred. No. 5.21e-122;
Matches 111; Conservative 10; Mismatches 22; Indels 0; Gaps 0;
Db 1 mwlgmllllgtvcsfsaptrpsvtrpwlvhdaikalsllndstdtaavmdetvev 60
|||||
Qy 1 mwlgslillgtvacsisaprspsqpwelhmaiqearllnlsrdtaamnetvev 60
|||||
Db 61 semfdsqepctcltrlelykqglrsgitklkplmtmashyqhpcptpsetcatqitf 120
|||||
Qy 61 semfdlqepctcltrlelykqglrsgitklkplmtmashyqhpcptpsetcatqitf 120
|||||
Db 121 ksfkenlkdfllvxfdcwepvq 143
|||||
Qy 121 esfkenlkdfllvxfdcwepvq 143
|||||
RESULT 3

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Jun 21 12:09

/home/pandya/mertz_08_466_308/P60535.rpr

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```

ENTRY      A61632      #type complete
TITLE      granulocyte-macrophage colony-stimulating factor precursor -
ORGANISM    sheep
            #formal name Ovis orientalis aries, Ovis ammon aries
            #common name domestic sheep
DATE        21-Jul-1995 #sequence_revision 28-Jul-1995 #text_change
            28-Jul-1995
ACCESSIONS  A61632
REFERENCE    A61632
            #authors O'Brien, P.M.; Rothel, J.S.; Seow, H.F.; Wood, P.R.
            #journal Immunol. Cell Biol. (1991) 69:51-55
            #title Cloning and sequencing of the cDNA for ovine
            granulocyte-macrophage colony-stimulating factor (GM-CSF).
            #accession A61632
            #status preliminary; not compared with conceptual translation
            #molecule_type mRNA
            #residues 1-144 ##label OAB
FEATURE
1-17        #domain signal sequence #status predicted #label SIG
SUMMARY     #length 144 #molecular-weight 16290 #checksum 8953
Query Match 81.4%; Score 821; DB 11; Length 144;
Best Local Similarity 76.9%; Pred. No. 9,19e-121;
Matches 110; Conservative 10; Mismatches 23; Indels 0; Gaps 0;
Db 1 mwlglllgtvcsfsaptrpqrhwqvdaikealslndstdtaavmdetvev 60
    |||||:||||| ||||| ||||| :||:||||| || ||||| :|||||
Qy 1 mwlgslllgtvacsisapxrspsxqpwelhvnaigearllnlsrdtaaxnetvev 60
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 61 semfdseptcltrlelykqglrgsltslmtmashykhkcpptgscetqitf 120
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 61 semfdlqptcltrlelykqglrgsltslmtmashykhkcpptgscatqitf 120
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 121 ksfenlkdfllvxfdcwepvq 143
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 121 esfkenlkdfllvxfdcwepvq 143
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
RESULT      4
ENTRY      F0BOGM      #type complete
TITLE      granulocyte-macrophage colony-stimulating factor precursor -
            bovine
ALTERNATE_NAMES  colony-stimulating factor 2; GM-CSF
ORGANISM      #formal name Bos primigenius taurus #common name cattle
DATE          31-Mar-1989 #sequence_revision 31-Mar-1989 #text_change
            27-Jan-1995
ACCESSIONS  J10037
REFERENCE    J10037
            #authors Maliszewski, C.R.; Schoenborn, M.A.; Cerretti, D.P.; Wignall,
            J.M.; Picha, K.S.; Cosman, D.; Tushinski, R.J.; Gillis, S.;
            Baker, P.E.
            #journal Mol. Immunol. (1988) 25:843-850
            #title Bovine GM-CSF: molecular cloning and biological activity of
            the recombinant protein.
            #cross-references MUID:89096971
            #accession J10037
            #molecule_type mRNA
            #residues 1-143 ##label MAL
COMMENT      This glycoprotein induces granulocyte, macrophage, and eosinophil
            colony formation.
CLASSIFICATION #superfamily granulocyte-macrophage colony-stimulating factor
KEYWORDS      cytokine; glycoprotein; growth factor; macrophage; monomer;
            T-cell
FEATURE

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/home/pandya/mertz_08_466_308/P60535.rpr

6

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1-17        #domain signal sequence #status predicted #label SIG
18-143      #product granulocyte-macrophage colony-stimulating
            factor #status predicted #label MAL
44,54       #binding site carbohydrate (Asn) (covalent) #status
            predicted
SUMMARY     #length 143 #molecular-weight 16157 #checksum 5779
Query Match 76.7%; Score 773; DB 2; Length 143;
Best Local Similarity 69.2%; Pred. No. 3.14e-112;
Matches 99; Conservative 20; Mismatches 23; Indels 1; Gaps 1;
Db 1 mwlglllgtvcsfsaptrpqrhwqvdaikealslndstdtdavmdet-evv 59
    |||||:||||| ||||| ||||| :||:||||| || ||||| ||||| |||||
Qy 1 mwlgslllgtvacsisapxrspsxqpwelhvnaigearllnlsrdtaaxnetvev 60
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 60 sekfdseptcltrlelyknglqgsltslmtmashykhkcpptgscetqitf 119
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 61 semfdlqptcltrlelykqglrgsltslmtmashykhkcpptgscatqitf 120
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 120 knfkedkeflfiipfdwepaq 142
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 121 esfkenlkdfllvxfdcwepvq 143
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
RESULT      5
ENTRY      A44936      #type complete
TITLE      granulocyte-macrophage colony-stimulating factor, GM-CSF -
            dog
ORGANISM      #formal name Canis lupus familiaris #common name dog
DATE          17-Feb-1994 #sequence_revision 17-Feb-1994 #text_change
            12-Apr-1995
ACCESSIONS  A44936
REFERENCE    A44936
            #authors Nash, R.A.; Schuening, F.; Appelbaum, F.; Hammond, W.P.;
            Boone, T.; Morris, C.F.; Slichter, S.J.; Storb, R.
            #journal Blood (1991) 78:930-937
            #title Molecular cloning and in vivo evaluation of canine
            granulocyte-macrophage colony-stimulating factor.
            #cross-references MUID:91329842
            #accession A44936
            #status preliminary
            #molecule_type mRNA
            #residues 1-144 ##label NAS
            #cross-references NCBI:49738; NCBI:49739
            #note sequence extracted from NCBI backbone
CLASSIFICATION #superfamily granulocyte-macrophage colony-stimulating factor
SUMMARY     #length 144 #molecular-weight 16137 #checksum 9761
Query Match 74.6%; Score 752; DB 5; Length 144;
Best Local Similarity 69.7%; Pred. No. 1.67e-108;
Matches 99; Conservative 17; Mismatches 26; Indels 0; Gaps 0;
Db 1 mwlglllgtvcsfsaptrpqrhwqvdaikealslndstdtaavmkaevv 60
    |||||:||||| ||||| ||||| :||:||||| ||||| ||||| ||||| |||||
Qy 1 mwlgslllgtvacsisapxrspsxqpwelhvnaigearllnlsrdtaaxnetvev 60
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 61 sevfdseptcltrlelykqglrgsltslmtmashykhkcpptgscatqitf 120
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 61 semfdlqptcltrlelykqglrgsltslmtmashykhkcpptgscatqitf 120
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 121 ksfenlkdfllvxfdcwepv 142
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 121 esfkenlkdfllvxfdcwepv 142
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

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RESULT      6
ENTRY       A24644      #type complete
TITLE       granulocyte-macrophage colony-stimulating factor precursor -
            mouse
ALTERNATE_NAMES
ORGANISM     colony-stimulating factor 2; GM-CSF
              #formal name Mus musculus #common name house mouse
DATE        22-Jul-1987 #sequence_revision 22-Jul-1987 #text_change
            18-Jun-1993
ACCESSIONS  A24644
REFERENCE   A24644
AUTHORS     Delamarter, J.F.; Mermod, J.J.; Liang, C.M.; Eliason, J.F.;
            Thatcher, D.R.
JOURNAL     EMBO J. (1985) 4:2575-2581
CROSS-REFERENCES MUID:86030236
ACCESSION  A24644
MOLECULE_TYPE mRNA
RESIDUES    1-141 ##label DEL
CLASSIFICATION
SUPERFAMILY superfamily granulocyte-macrophage colony-stimulating factor
KEYWORDS     cytokine; glycoprotein; growth factor; macrophage; monomer;
            T-cell
SUMMARY      #length 141 #molecular-weight 16133 #checksum 4526

Query Match      54.2%; Score 546; DB 5; Length 141;
Best Local Similarity 53.1%; Pred. No. 2.53e-72;
Matches 76; Conservative 20; Mismatches 44; Indels 3; Gaps 1;

Db 1 mwlgmllfigivvyslsaptrspitvrpkhveakealnllid---dmpvthneevv 57
      ||||:||||| | |:||| ||| :|||:||||| | | | ||||| || | |
Qy 1 mwlgslilgtvacsisapxrspsxqpwelhvaigearrllnlsrdaexnetvevx 60
      ||||:||||| | |:||| ||| :|||:||||| | | | ||||| || | |

Db 58 snefskklctvqrklifegqlrgnftklkgalntasytycypptdctqvtty 117
      | : | : ||:|||| : |||:|||||: | | | ||||| || | | :
Qy 61 semfdlqptclqrllykqglqsltkkqplmtmaashykhqcpptscatqkitf 120
      | : || | | ||| | | | | | | | | | | | | | | | | | |

Db 118 adfidslktfltdipfeckpqq 140
      | : || | | ||| | | | | | | | | | | | | | | | | | |
Qy 121 esfkenlkdfllvxpfdwepvq 143
      | : || | | ||| | | | | | | | | | | | | | | | | | |

RESULT      7
ENTRY       A24636      #type complete
TITLE       granulocyte-macrophage colony-stimulating factor precursor -
            mouse
ALTERNATE_NAMES
ORGANISM     colony-stimulating factor 2; GM-CSF
              #formal name Mus musculus #common name house mouse
DATE        22-Jul-1987 #sequence_revision 22-Jul-1987 #text_change
            14-Sep-1994
ACCESSIONS  A24636; A24645
REFERENCE   A91015
AUTHORS     Miyatake, S.; Otsuka, T.; Yokota, T.; Lee, F.; Arai, K.
JOURNAL     EMBO J. (1985) 4:2561-2568
TITLE       Structure of the chromosomal gene for granulocyte-macrophage
            colony stimulating factor: comparison of the mouse and
            human genes.
CROSS-REFERENCES MUID:86030234
ACCESSION  A24636
MOLECULE_TYPE DNA; mRNA
RESIDUES    1-141 ##label M1Y
NOTE        the sequence translated from the mRNA differs from that
            of the DNA in having 139-Ser
REFERENCE   A24645
AUTHORS     Stanley, E.; Metcalf, D.; Sobieszczuk, P.; Gough, N.M.; Dunn,
            A.R.

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JOURNAL     EMBO J. (1985) 4:2569-2573
TITLE       The structure and expression of the murine gene encoding
            granulocyte-macrophage colony stimulating factor: evidence
            for utilisation of alternative promoters.
CROSS-REFERENCES MUID:86030235
ACCESSION  A24645
MOLECULE_TYPE DNA
RESIDUES    1-141 ##label STA
GENETICS
INTRONS     50/3; 64/3; 106/3
CLASSIFICATION
SUPERFAMILY superfamily granulocyte-macrophage colony-stimulating factor
KEYWORDS     cytokine; glycoprotein; growth factor; macrophage; monomer;
            T-cell
SUMMARY      #length 141 #molecular-weight 16090 #checksum 4151

Query Match      53.2%; Score 536; DB 5; Length 141;
Best Local Similarity 52.4%; Pred. No. 1.37e-70;
Matches 75; Conservative 20; Mismatches 45; Indels 3; Gaps 1;

Db 1 mwlgmllfigivvyslsaptrspitvrpkhveakealnllid---dmpvthneevv 57
      ||||:||||| | |:||| ||| :|||:||||| | | | ||||| || | |
Qy 1 mwlgslilgtvacsisapxrspsxqpwelhvaigearrllnlsrdaexnetvevx 60
      ||||:||||| | |:||| ||| :|||:||||| | | | ||||| || | |

Db 58 snefskklctvqrklifegqlrgnftklkgalntasytycypptdctqvtty 117
      | : | : ||:|||| : |||:|||||: | | | ||||| || | | :
Qy 61 semfdlqptclqrllykqglqsltkkqplmtmaashykhqcpptscatqkitf 120
      | : || | | ||| | | | | | | | | | | | | | | | | | |

Db 118 adfidslktfltdipfeckpqq 140
      | : || | | ||| | | | | | | | | | | | | | | | | | |
Qy 121 esfkenlkdfllvxpfdwepvq 143
      | : || | | ||| | | | | | | | | | | | | | | | | | |

RESULT      8
ENTRY       F0MSGM      #type complete
TITLE       granulocyte-macrophage colony-stimulating factor - mouse
ALTERNATE_NAMES
ORGANISM     colony-stimulating factor 2; GM-CSF
              #formal name Mus musculus #common name house mouse
DATE        28-Aug-1985 #sequence_revision 28-Aug-1985 #text_change
            10-Mar-1994
ACCESSIONS  A01854
REFERENCE   A01854
AUTHORS     Gough, N.M.; Gough, J.; Metcalf, D.; Kelso, A.; Graill, D.;
            Nicola, N.A.; Butgess, A.W.; Dunn, A.R.
JOURNAL     Nature (1984) 309:763-767
TITLE       Molecular cloning of cDNA encoding a murine haematopoietic
            growth regulator, granulocyte-macrophage colony stimulating
            factor.
CROSS-REFERENCES MUID:84245825
ACCESSION  A01854
MOLECULE_TYPE mRNA
RESIDUES    1-118 ##label G0U
CROSS-REFERENCES GB:X05906
COMMENT      The mRNA for this protein was isolated from lung tissue.
CLASSIFICATION
SUPERFAMILY superfamily granulocyte-macrophage colony-stimulating factor
KEYWORDS     cytokine; glycoprotein; growth factor; macrophage; monomer;
            T-cell
FEATURE
FEATURE_1    60,69      #binding site carbohydrate (Asn) (covalent) #status
                   predicted
SUMMARY      #length 118 #molecular-weight 13544 #checksum 2606

Query Match      41.3%; Score 416; DB 2; Length 118;
Best Local Similarity 50.9%; Pred. No. 5.37e-50;
Matches 59; Conservative 17; Mismatches 37; Indels 3; Gaps 1;

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Db 499 llglgitagtgtstalikgpi-dlqqgltslqiaidadlralqdsvkledsltsls 555
||| :: :: | : : : ||| : || :: ||| :: || ::
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Jun 21 12:09 /home/pandya/mertz_08_466_308/P60535.rpr 13

Oy 42 llnlsrdaexnetvevxsemfdlqep-tclqtrlelykqglqgsitkklqplmma 98

Search completed: Fri Jun 21 12:19:43 1996
Job time : 17 secs.

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